

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/006,797

Source: 1Fw16

Date Processed by STIC: 3/9/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/09/2005

PATENT APPLICATION: US/10/006,797

TIME: 11:21:15

Input Set : A:\12669-002001.TXT

Output Set: N:\CRF4\03092005\J006797.raw

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4 <110> APPLICANT: Fraser, John David
5     Nicholson, Melissa Joy
8 <120> TITLE OF INVENTION: Immunomodulatory Constructs And Their
9     Uses
11 <130> FILE REFERENCE: 12669-002001
13 <140> CURRENT APPLICATION NUMBER: US 10/006,797
14 <141> CURRENT FILING DATE: 2001-12-04
16 <150> PRIOR APPLICATION NUMBER: US 60/251,243
17 <151> PRIOR FILING DATE: 2000-12-04
19 <160> NUMBER OF SEQ ID NOS: 22
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 621
25 <212> TYPE: DNA
26 <213> ORGANISM: Streptococcus pyogenes
28 <400> SEQUENCE: 1
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30 ccttatgatt ataaagattg cagggtaaat ttttcaacga cacacacatt aaacattgat 120
31 actcaaaaat atagagggaa agactattat attagttccg aaatgtctta tgaggcctct 180
32 caaaaattta aacgagatga tcatgtagat gtttttggat tattttatat tcttaattct 240
33 cacaccggtg agtacatcta tggaggaatt acgcctgctc aaaataataa agtaaattcat 300
34 aaattattgg gaaatctatt tatttcggga gaatctcaac agaacttaaa taacaagatt 360
35 attctagaaa aggatatcgt aactttccag gaaattgact ttaaaatcag aaaatacctt 420
36 atggataatt ataaaattta tgacgctact tctccttatg taagcggcag aatcgaaatt 480
37 ggcacaaaag atgggaaaca tgagcaaata gacttatttg actcacaaa tgaagggact 540
38 agatcagata tttttgcaaa atataaagat aatagaatta tcaatatgaa gaactttagt 600
39 catttcgata tttatcttga a
601
41 <210> SEQ ID NO: 2
42 <211> LENGTH: 207
43 <212> TYPE: PRT
44 <213> ORGANISM: Streptococcus pyogenes
46 <400> SEQUENCE: 2
47 Asp Ser Lys Lys Asp Ile Ser Asn Val Lys Ser Asp Leu Leu Tyr Ala
48 1 5 10 15
49 Tyr Thr Ile Thr Pro Tyr Asp Tyr Lys Asp Cys Arg Val Asn Phe Ser
50 20 25 30
51 Thr Thr His Thr Leu Asn Ile Asp Thr Gln Lys Tyr Arg Gly Lys Asp
52 35 40 45
53 Tyr Tyr Ile Ser Ser Glu Met Ser Tyr Glu Ala Ser Gln Lys Phe Lys
54 50 55 60
55 Arg Asp Asp His Val Asp Val Phe Gly Leu Phe Tyr Ile Leu Asn Ser
56 65 70 75 80
57 His Thr Gly Glu Tyr Ile Tyr Gly Gly Ile Thr Pro Ala Gln Asn Asn

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58          85          90          95
59 Lys Val Asn His Lys Leu Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser
60          100          105          110
61 Gln Gln Asn Leu Asn Asn Lys Ile Ile Leu Glu Lys Asp Ile Val Thr
62          115          120          125
63 Phe Gln Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu Met Asp Asn Tyr
64          130          135          140
65 Lys Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile
66 145          150          155          160
67 Gly Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro
68          165          170          175
69 Asn Glu Gly Thr Arg Ser Asp Ile Phe Ala Lys Tyr Lys Asp Asn Arg
70          180          185          190
71 Ile Ile Asn Met Lys Asn Phe Ser His Phe Asp Ile Tyr Leu Glu
72          195          200          205
75 <210> SEQ ID NO: 3
76 <211> LENGTH: 621
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Mutant from Streptococcus pyogenes
83 <400> SEQUENCE: 3
84 gactctaaga aagacatttc gaatgttaaa agtgatttac tttgtgcata cactataact 60
85 ccttatgatt ataaagattc cagggtaaat ttttcaacga cacacacatt aaacattgat 120
86 actcaaaaat atagagggaa agactattat attagtccg aaatgtctta tgaggcctct 180
87 caaaaattta aacgagatga tcatgtagat gtttttgat tattttatat tctttgttct 240
88 cacaccggtg agtacatcta tggaggaatt acgcctgctc aaaataataa agtaaatcat 300
89 aaattattgg gaaatctatt ttttcggga gaatctcaac agaacttaaa taacaagatt 360
90 attctagaaa aggatatcgt aactttccag gaaattgact ttaaaatcag aaaatacctt 420
91 atggataatt ataaaattta tgacgctact tctccttatg taagcggcag aatcgaaatt 480
92 ggcacaaaag atgggaaaca tgagcaaata gacttatttg actcacaaa tgaaggggact 540
93 caatcgata tttttgcaaa atataaagat aatagaatta tcaatatgaa gaactttagt 600
94 catttcgata tttatcttga a 621
96 <210> SEQ ID NO: 4
97 <211> LENGTH: 207
98 <212> TYPE: PRT
99 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Mutant from Streptococcus pyogenes
104 <400> SEQUENCE: 4
105 Asp Ser Lys Lys Asp Ile Ser Asn Val Lys Ser Asp Leu Leu Ala Ala
106 1 5 10 15
107 Tyr Thr Ile Thr Pro Tyr Asp Tyr Lys Asp Ser Arg Val Asn Phe Ser
108 20 25 30
109 Thr Thr His Thr Leu Asn Ile Asp Thr Gln Lys Tyr Arg Gly Lys Asp
110 35 40 45
111 Tyr Tyr Ile Ser Ser Glu Met Ser Tyr Glu Ala Ser Gln Lys Phe Lys
112 50 55 60
113 Arg Asp Asp His Val Asp Val Phe Gly Leu Phe Tyr Ile Leu Cys Ser

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114 65          70          75          80
115 His Thr Gly Glu Tyr Ile Tyr Gly Gly Ile Thr Pro Ala Gln Asn Asn
116          85          90          95
117 Lys Val Asn His Lys Leu Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser
118          100          105          110
119 Gln Gln Asn Leu Asn Asn Lys Ile Ile Leu Glu Lys Asp Ile Val Thr
120          115          120          125
121 Phe Gln Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu Met Asp Asn Tyr
122          130          135          140
123 Lys Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile
124 145          150          155          160
125 Gly Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro
126          165          170          175
127 Asn Glu Gly Thr Gln Ser Asp Ile Phe Ala Lys Tyr Lys Asp Asn Arg
128          180          185          190
129 Ile Ile Asn Met Lys Asn Phe Ser His Phe Asp Ile Tyr Leu Glu
130          195          200          205
133 <210> SEQ ID NO: 5
134 <211> LENGTH: 432
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial Sequence
138 <220> FEATURE:
139 <223> OTHER INFORMATION: Synthetic construct
141 <220> FEATURE:
142 <221> NAME/KEY: CDS
143 <222> LOCATION: (1)...(429)
145 <400> SEQUENCE: 5
146 gac tct aag aaa gac att tcg aat gtt aaa agt gat tta ctt tgc gca 48
147 Asp Ser Lys Lys Asp Ile Ser Asn Val Lys Ser Asp Leu Leu Cys Ala
148 1          5          10          15
150 tac act ata act cct atc gaa ggt cgt acg cct gct caa aat aat aaa 96
151 Tyr Thr Ile Thr Pro Ile Glu Gly Arg Thr Pro Ala Gln Asn Asn Lys
152          20          25          30
154 gta aat cat aaa tta ttg gga aat cta ttt att tcg gga gaa tct caa 144
155 Val Asn His Lys Leu Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser Gln
156          35          40          45
158 cag aac tta aat aac aag att att cta gaa aag gat acc gta act ttc 192
159 Gln Asn Leu Asn Asn Lys Ile Ile Leu Glu Lys Asp Thr Val Thr Phe
160          50          55          60
162 cag gaa att gac ttt aaa atc aga aaa tac ctt atg gat aat tat aaa 240
163 Gln Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu Met Asp Asn Tyr Lys
164 65          70          75          80
166 att tat gac gct act tct cct tat gta agc ggc aga atc gaa att ggc 288
167 Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile Gly
168          85          90          95
170 aca aaa gat gga aaa cat gag caa ata gac tta ttt gac tca cca aat 336
171 Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro Asn
172          100          105          110
174 gaa ggg act aga tca gat att ttt gca aaa tat aaa gat aat aga att 384

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175 Glu Gly Thr Arg Ser Asp Ile Phe Ala Lys Tyr Lys Asp Asn Arg Ile
176          115          120          125
178 atc aat atg aag aac ttt agt cat ttc gat att tat ctt gaa aaa      429
179 Ile Asn Met Lys Asn Phe Ser His Phe Asp Ile Tyr Leu Glu Lys
180      130          135          140
182 taa      432
184 <210> SEQ ID NO: 6
185 <211> LENGTH: 143
186 <212> TYPE: PRT
187 <213> ORGANISM: Artificial Sequence
189 <220> FEATURE:
190 <223> OTHER INFORMATION: Synthetic construct
192 <400> SEQUENCE: 6
193 Asp Ser Lys Lys Asp Ile Ser Asn Val Lys Ser Asp Leu Leu Cys Ala
194  1          5          10          15
195 Tyr Thr Ile Thr Pro Ile Glu Gly Arg Thr Pro Ala Gln Asn Asn Lys
196          20          25          30
197 Val Asn His Lys Leu Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser Gln
198          35          40          45
199 Gln Asn Leu Asn Asn Lys Ile Ile Leu Glu Lys Asp Thr Val Thr Phe
200      50          55          60
201 Gln Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu Met Asp Asn Tyr Lys
202 65          70          75          80
203 Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile Gly
204          85          90          95
205 Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro Asn
206          100          105          110
207 Glu Gly Thr Arg Ser Asp Ile Phe Ala Lys Tyr Lys Asp Asn Arg Ile
208          115          120          125
209 Ile Asn Met Lys Asn Phe Ser His Phe Asp Ile Tyr Leu Glu Lys
210      130          135          140
213 <210> SEQ ID NO: 7
214 <211> LENGTH: 25
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Primers
221 <400> SEQUENCE: 7
222 cgggatccga ctctcaagaa agaca      25
224 <210> SEQ ID NO: 8
225 <211> LENGTH: 22
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Primers
232 <400> SEQUENCE: 8
233 ctgaattctt atttttcaag at      22
235 <210> SEQ ID NO: 9
236 <211> LENGTH: 20

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237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Primers
243 <400> SEQUENCE: 9
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246 <210> SEQ ID NO: 10
247 <211> LENGTH: 18
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Primers
254 <400> SEQUENCE: 10
255 atattctttg ttctcaca 18
257 <210> SEQ ID NO: 11
258 <211> LENGTH: 20
259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial Sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: Primer
265 <400> SEQUENCE: 11
266 gatttacttt gtgcatacac 20
268 <210> SEQ ID NO: 12
269 <211> LENGTH: 26
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Primer
276 <400> SEQUENCE: 12
277 gaagggactc aatcagatat ttttgc 26
279 <210> SEQ ID NO: 13
280 <211> LENGTH: 34
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Primer
287 <400> SEQUENCE: 13
288 atcgaaggtc gtacgcctgc tcaaaataat aaag 34
290 <210> SEQ ID NO: 14
291 <211> LENGTH: 22
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
296 <223> OTHER INFORMATION: Primer
298 <400> SEQUENCE: 14
299 gattataaag attccagggt aa 22
301 <210> SEQ ID NO: 15
302 <211> LENGTH: 20
303 <212> TYPE: DNA

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VERIFICATION SUMMARY

PATENT APPLICATION: **US/10/006,797**

DATE: 03/09/2005

TIME: 11:21:16

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